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3. (Amended) The method of Claim 1 wherein said non-coding region [intron] sequence is adjacent to an exon encoding said allele.

6. (Amended) The method of Claim 5 wherein said amplified DNA sequence includes at least about 1,000 nucleotides corresponding to non-coding region [intron] sequences.

7. (Amended) A method for detection of at least one allele of a multi-allelic genetic locus comprising:

a) amplifying genomic DNA with a [an intron-spanning] primer pair that spans a non-coding region sequence, said primer pair defining [that defines] a DNA sequence which is [, said DNA sequence being] in genetic linkage with said allele and contains [containing] a sufficient number of non-coding region [intron] sequence nucleotides to produce an amplified DNA sequence characteristic of said allele; and

b) analyzing said amplified DNA sequence to detect the presence of a genetic variation in said amplified sequence.

15. (Amended) The method of Claim 7 wherein at least about 70% of said primer-defined amplified DNA sequence corresponds to non-coding region [intron] sequences.

17. (Amended) A method for producing RFLP fragments characteristic of alleles of [for] an HLA locus of an individual comprising the steps of:

a) amplifying genomic HLA DNA from said individual with a primer pair specific for said HLA locus under conditions suitable to produce an amplified DNA sequence; and

b) producing a digest by combining said amplified DNA sequence with at least one endonuclease that cleaves said amplified DNA sequence to yield a set of fragments having distinctive fragment lengths.

Add the following new claims.

35. The method of Claim 1 wherein said genetic locus has at least four alleles.

36. The method of Claim 1 wherein said genetic locus has at least eight alleles.

36. An improved DNA analysis method in which coding region alleles of a multi-allelic genetic locus are determined by identifying sequence polymorphisms characteristic of the alleles, the improvement comprising identifying sequence polymorphisms characteristic of the alleles in a non-coding region sequence, said non-coding region sequence being not more than about two kilobases in length.

37. The method of Claim 36 wherein said non-coding region sequence is not more than about one kilobase in length.

38. The method of Claim 36 wherein said sequence polymorphisms characteristic of the alleles are within five kilobases of a variable exon of the genetic locus.

39. The method of Claim 36 wherein said sequence polymorphisms characteristic of the alleles are within two kilobases of a variable exon of the genetic locus.

40. The method of Claim 36 wherein said sequence polymorphism characteristic of said coding region allele is present in an intervening sequence adjacent to a variable exon of the locus.

41. The method of Claim 40 wherein the genetic locus is an HLA Class I locus and the intervening sequence is intervening sequence  $\frac{I}{1}, \frac{II}{2}, \frac{III}{3}$  or  $\frac{I}{4}, \frac{II}{5}$ .

42. The method of Claim 40 wherein the genetic locus is an HLA Class II locus and the intervening sequence is intervening sequence  $\frac{I}{1}, \frac{II}{2}$  or  $\frac{II}{1}, \frac{I}{2}$ .